



Release 3.1A John F. Collins, Biocomputing Research Unit.

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MPsrch_pp protein - protein database search,

using Smith-Waterman algorithm

Run on: Wed Mar 8 10:23:17 2000; MasPar time 10.58 Seconds

601.178 Million cell updates/sec

Tabular output not generated.

Title: >US-09-163-445-1

Description: (1-13) from US09163445.pep

Perfect Score: 1544

Sequence: 1 MATIVILLLAVLGSIPSGL.....NKTENIWPWGLNTHDPRKK 213

scoring table: PAM 150

Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot38

1:swissprot

Statistics: Mean 48.353; Variance 138.901; scale 0.348

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	Pred. No.
1	1536	YPAE STRN	YPAE	213	1	HYPOTHETICAL	23.0 KD P
2	616	YNE5_BACSU	YNE5	193	1	HYPOTHETICAL	21.0 KD P
3	460	Y676_AQUR	Y676	192	1	HYPOTHETICAL	20.9 KD P
4	354	SYN3	SYN3	222	1	HYPOTHETICAL	23.5 KD P
5	297	YGH1_ECOLI	YGH1	205	1	HYPOTHETICAL	22.2 KD P
6	294	YGH1_HAEIN	YGH1	199	1	HYPOTHETICAL	21.7 KD P
7	256	YF09_HELPY	YF09	262	1	HYPOTHETICAL	21.6 KD P
8	188	Y247_MYCCE	Y247	122	1	HYPOTHETICAL	17.5 KD P
9	158	Y247_MYCCE	Y247	102	1	HYPOTHETICAL	16.6 KD P
10	145	YAH1_MOUSE	YAH1	80	1	SODIUM/HYDROGEN EXCHAN	23.0 KD P
11	142	YAH1_BOVIN	YAH1	92	1	SODIUM/HYDROGEN EXCHAN	9.7 KD P
12	142	YAH1_CRICR	YAH1	92	1	SODIUM/HYDROGEN EXCHAN	2.05e-03
13	141	YAH1_RABIT	YAH1	91	1	SODIUM/HYDROGEN EXCHAN	2.61e-03
14	140	YAH1_PIG	YAH1	91	1	SODIUM/HYDROGEN EXCHAN	3.31e-03
15	139	YAH1_RAT	YAH1	90	1	SODIUM/HYDROGEN EXCHAN	4.20e-03
16	137	SP2E_BACSU	SP2E	89	1	STAGE II SPORULATION P	6.74e-03
17	133	Y233_METJA	Y233	86	1	URACIL PERMEASE (URACI	1.72e-02
18	132	YMBM_YEAST	YMBM	85	1	HYPOTHETICAL	5.9 KD P
19	129	YHAT_ECOLI	YHAT	84	1	HYPOTHETICAL	43.0 KD P
20	130	Y609_METJA	Y609	84	1	HYPOTHETICAL	3.44e-02
21	127	ACRB_ECOLI	ACRB	82	1	ACRIFLAVIN RESISTANCE	6.84e-02
22	125	YH06_HAETN	YH06	81	1	PROBABLE TRANSPORT PRO	1.08e-01
23	125	NAH1_HUMAN	NAH1	81	1	SODIUM/HYDROGEN EXCHAN	1.08e-01

RESULT	1	YPAE_STRN	STANDARD;	PRT;	213 AA.
ID	YPAE_STRN				
AC	Q54916;				
DT	15-JUL-1999	(Rel. 38, Created)			
DT	15-JUL-1999	(Rel. 38, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	HYPOTHETICAL 23.0 KD PROTEIN IN PARE 5' REGION (OPRF2).				
OS	Streptococcus pneumoniae				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;				
[1]					
RN	SEQUENCE FROM N.A.				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=7785;				
RX	MEDLINE; 9312346.				
RA	PAN X.; FISHER M.;				
RT	"Cloning and characterization of the parC and parE genes of Streptococcus pneumoniae encoding DNA topoisomerase IV: role in fluoroquinolone resistance."				
RT	J. Bacteriol. 178:4069-4076 (1996).				
BL					
CC	-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).				
CC	-- SIMILARITY: BELONGS TO THE UPP0078 FAMILY.				

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CC -- SEQUENCE FROM N.A.

CC MEDLINE; 9312346.

RA PAN X.; FISHER M.;

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RT J. Bacteriol. 178:4069-4076 (1996).

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RT "Cloning and characterization of the parC and parE genes of Streptococcus pneumoniae encoding DNA topoisomerase IV: role in fluoroquinolone resistance."

RT J. Bacteriol. 178:4069-4076 (1996).

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RESULT 2 STANDARD; PRT; 193 AA.

ID YNFS-BACSU

AC 04064;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE HYPOTHETICAL 21.0 KD PROTEIN IN TLP-GRLB INTERGENIC REGION.

GN YNFS.

OS Bacillus subtilis.

OC Bacillus; Firmicutes; Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -1- SIMILARITY: BELONGS TO THE UPF0078 FAMILY.

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CC DR AE000701; AAC06869; 1;

CC KW Hypothetical protein; Transmembrane.

FT TRANSMEM 3 23 POTENTIAL.

FT TRANSMEM 51 71 POTENTIAL.

FT TRANSMEM 80 100 POTENTIAL.

FT TRANSMEM 112 132 POTENTIAL.

FT TRANSMEM 149 169 POTENTIAL.

SQ SEQUENCE: CB757E2 CRC32;

Query Match 39.9%; Score 616; DB 1; Length 193;

Best Local Similarity 50.0%; Pred. No. 4.10e-65;

Matches 101; Conservative 45; Mismatches 46; Gaps 6;

Db 1 MLLALITLIALYLGICSPGLIVGKLAKTDIREHGSGNGLGNAFRTLGVRAGSVVTAQD 60

Qy 1 MITIVLILAYLGICSPGLIVGKLAKTDIREHGSGNGLGNAFRTLGVRAGSVVTAQD 60

Db 61 ILKGTLATLALPFLMHVD-1HPLLAGVFVAVLGHYPIFKEKGKAVATSGGVLFLYAPL 119

Qy 61 FFKGTLATLALPFLMHVD-1HPLLAGVFVAVLGHYPIFKEKGKAVATSGGVLFLYAPL 120

Db 120 FITRHFIFLYFLKFLVSSMGTGIVTIV---YS-F-FVTDY---LLIVVTL-TLIF 170

Qy 121 CYLAIIFGALYLGMSLSSVTASIAAVIGVLLPFLGFILSNYDSLFTAILALSL 180

Db 171 VIYRHRANIKRINTKTEPVK 192

Qy 181 IIIRHKDNIARIKRNTEVNPW 202

ID Y676-AQUAE STANDARD; PRT; 192 AA.

AC 066905;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE HYPOTHETICAL PROTEIN AQ_676.

GN AQ_676

OS Aquifex aeolicus.

OC Bacteria; Aquificales; Aquificaceae; Aquifex.

CC [1] RN

CC RP SEQUENCE FROM N.A.

CC RC STRAIN=VF5;

CC RX MEDLINE: 98196666.

CC RA DECKER G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;

CC RT "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus." Nature 392:353-358 (1998).

CC RT -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -1- SIMILARITY: BELONGS TO THE UPF0078 FAMILY.

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CC DR EMBL: AE000701; AAC06869; 1;

CC KW Hypothetical protein; Transmembrane.

FT TRANSMEM 3 23 POTENTIAL.

FT TRANSMEM 51 71 POTENTIAL.

FT TRANSMEM 80 100 POTENTIAL.

FT TRANSMEM 112 132 POTENTIAL.

FT TRANSMEM 149 169 POTENTIAL.

SQ SEQUENCE: CB757E2 CRC32;

Query Match 29.8%; Score 460; DB 1; Length 192;

Best Local Similarity 42.6%; Pred. No. 1.59e-43;

Matches 83; Conservative 55; Mismatches 43; Gaps 13;

Db 1 MKALFLYIFAVLGLSITFGEVIAKLK-GVDLRNVSGNYGATNYTRALGKKGYVLYFFLD 59

Qy 1 MIVVILILAYLGICSPGLIVGKLAKTDIREHGSGNGLGNAFRTLGVRAGSVVTAQD 60

Db 60 FLKGKIPALIAYKSGFSGIDS-WVLTGTLASVLYGHNMPVFGFKGKGVATLGTVAVSP 118

Qy 61 EFKGTLATLPLII-FHQLGYSPLIF-GLLAVIHTHEPIFAGFKGKGKAVATSGVFGFAP 118

Db 119 SVALFSPFLWVLG-INFUMKRYVSLASATIS-A-F-LFLFL-VAGTV-N--VLFMIVIG-170

Qy 119 IFCLYLAIITFGALYL-GSMISLSSVTASIAAVIGVLLPFLGFILSNYDSLFTAILAL 177

Db 171 A-LITYRHNTRNL 184

Qy 178 ASL1IIRHKDNIARI 192

RESULT 4 STANDARD; PRT; 222 AA.

ID YJ73-SYN 3

AC P73933;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE HYPOTHETICAL (23.5 KD PROTEIN SUL1973.

GN SUL1973.

OS Synchocystis sp. (strain PCC 6803);

OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.

CC [1] RN

CC RP SEQUENCE FROM N.A.

CC MEDLINE: 97061201.

RA	FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA	RA BURKHALD A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA	RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA	RA SCOTT J.D., SHIRLEY R., LIU L.T., GLODKE A., KELLEY J.M.,
RA	RA WIDMERBACK T.R., HANNA M.C., PHILLIPS C.A., SPRIGES T., HEDLØM E., COTTON M.D.,
RA	RA FINE L.D., Fritchman J.L., FURMANN J.L., GEOGRAPHEN N.S.M., SAUDEK D.M., BRANDON R.C.,
RA	RA GNEHM C.L., MCDONALD L.A., SHALD K.V., FRASER C.M., SMITH H.O.,
RA	RA VENTER J.C.;
RT	RT Whole-genome random sequencing and assembly of <i>Haemophilus</i>
RT	RT <i>Influenzae</i> Rd.;
RT	RT Science 269: 496-512(1995).
CC	CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC	CC -1 SIMILARITY: BELONGS TO THE UPP078 FAMILY. STRONG, TO E.COLI YGIH.
CC	CC
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	CC
DR	DR EMBL: U32713; AAC21932.1; -.
DR	DR TIGR: H10266; -.
KW	KW HYPOTHETICAL protein; Transmembrane.
FT	FT TRANSMEM 4 24 POTENTIAL.
FT	FT TRANSMEM 56 76 POTENTIAL.
FT	FT TRANSMEM 80 100 POTENTIAL.
FT	FT TRANSMEM 115 135 POTENTIAL.
FT	FT TRANSMEM 138 158 POTENTIAL.
SQ	SQ SEQUENCE 199 AA; 22113 MW; 31409562 CRC32;
Query Match	Score 294; DB 1; Length 199;
Best Local Similarity	35.3%;
Matches	72; Conservative 52; Mismatches 67; Indels 13; Gaps 10
Db	3 LFALPFMLAYLGGSSSAAATLICRAGLPPDPRQNSHNPAGATVNLIGNRKSALAVLIFD 62
Qy	1 MTTIVLILAYLGLGSPGMIGQVFFQINLRESGNTGTTNTFRLGKAGNATFVID 60
Db	63 MLRGMNPWVAGYYLGLTQELFGMVAQAGLGHIPFFQPKGGKYATAFGAI---APF- 118
Qy	61 FFKGTATLPLIPIHFGQGSPLIFGLAVTIGHTFPFAGFKGGRAVATSGVTFGPAPIF 120
Db	119 SWAVAGSMFTGWI-FVFLYSGKSSLSAVISALLYP-F-YVWW FKPEF-TFPVAVCVC 171
Qy	121 CLYATIIFPAFLGQMSIISLSSVPAASIAAVGVLJLPLFESLNSYDSDSFLIAAS- 179
Db	172 LLYIYRHDNFIORLWRQEDKV-WA 194
Qy	180 LIIIRHKDNIAKRNKTNLYPVG 203
RESULT	7
ID	HELPY STANDARD; PRT; 262 AA.
AC	AC 026039;
DT	DT 15-JUL-1999 (Rel. 38, Created)
DT	DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT	DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE	DE HYPOTHETICAL PROTEIN HP1509.
GN	GN HP1509.
OS	OS Helicobacter pylori (Campylobacter pylori).
OC	OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC	OC Helicobacter.
RN	RN [1]
RP	RP SEQUENCE FROM N-A.
RC	RC STRAN=2665 / ATCC 700392;
RX	RX MEDLINE; 97394467.
RA	RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
RA	RA KLENK H.-P., GILL S., DOUGHERTY B.A.,
RA	RA FLEISCHMANN R.D., KETCHUM K.A., ZODKEVICH J., ZODKEVICH J., KIRKNESS E.F., PETERSON S.,
RA	RA NELSON K., QUACKENBUSH J., ZODKEVICH J., KIRKACK H.G., GLODEK A.,
RA	RA LOFTUS B., RICHARDSON D., DODSON R., KIRKACK H.G., GLODEK A.,

MCKENNEY K., FITZGERALD L.M., LEW N., ADAMS M.D., HICKIE E.K., RA BERG D.E., GOCAINE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M., RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEW L., WALLIN E., RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M., RA VENTER J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter pylori."
RL [Nature 388:539-547 \(1997\)](http://www.ncbi.nlm.nih.gov/entrez/pmc/article.cgi?pmid=97197)
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE UP0078 FAMILY.
CC
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CC
CC DR EMBL: AE000649; AAD08551; 1; -.
CC DR TIGR: HP1509; -.
CC KW Hypothetical protein; Transmembrane.
CC FT 53 73 POTENTIAL.
CC TRANSMEM
CC FT 96 96 POTENTIAL.
CC TRANSMEM
CC FT 112 132 POTENTIAL.
CC TRANSMEM
CC FT 170 190 POTENTIAL.
CC TRANSMEM
CC FT 195 215 POTENTIAL.
CC SEQUENCE: 262 AA; 28835 MW; 5CE61FE3 CRC32;
CC
Query Match 16 68; Score 256; DB 1; Length 262;
Best Local Similarity 33.1%; Pred. No. 1.13e-16;
Matches 54; Conservative 48; Mismatches 50; Indels 11; Gaps 9;
CC
Db 53 INVIFTLGLIGGIPFGYALMKIFGMDTITKIGSGIGATNVLQALSGVSNAKOMAL 112
Qy 2 ITIVLVLJAYLJGSGIPSGLNGQVFOINERHGSGNTCTNTFIL-GR--KA-GMAT 56
Db 113 LVLIDLFLKGNAFVLFLSKLFGIDSYLQWVMAIASTLGHYCKSPFLNFGKVSTIMGSVY 172
Qy 57 FV-I-DEFKGTLATLFLPFLPFLGQSPFLFLLAVGHTPFLFAGFKGGKAVATSGVIF 114
Db 173 LIPPIESLIGLTWTFVKGKL-IKSSLASLIG-VGATF-VLIF 212
Qy 115 GFAPIFCLY-LAIIFFGALYLGMSLSSY-TASIAVIGVLF 156
CC
RESULT 8
ID Y247 MYCCE STANDARD: PRT: 239 AA.
AC P47489;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOTHETICAL PROTEIN MG247.
DN MG247.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 334530 / G-37;
RX MEDLINE; 96126316.
RA FRASER C.M., GOCAINE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,
RA FLEISCHMANN R., BULT C.J., KERLAWAIGE A.R., SUTTON G., KELLEY J.M.,
RA FRITCHMAN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHRMANN J.L.,
RA NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M.,
RA TAMB J.-F., DOUGHERTY B.A., BOTT K.P., HU P.-C., LUCIER T.S.,
RA PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.,
RA "The minimal gene complement of Mycoplasma genitalium."
RL [Science 270:397-403 \(1995\)](http://www.ncbi.nlm.nih.gov/entrez/pmc/article.cgi?pmid=7039403).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE UP0078 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

FT	DOMAIN	184	188	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	189	210	E (N5) (POTENTIAL).	
FT	DORAIN	211	230	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	231	251	F (N5A) (POTENTIAL).	
FT	DORAIN	252	260	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	261	282	G (N5B) (POTENTIAL).	
FT	DORAIN	283	301	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	302	322	H (N6) (POTENTIAL).	
FT	DORAIN	323	336	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	337	357	I (N7) (POTENTIAL).	
FT	DORAIN	358	388	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	389	410	J (N8) (POTENTIAL).	
FT	DORAIN	411	416	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	417	438	K (N9) (POTENTIAL).	
FT	DORAIN	439	452	EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN	453	473	L, HYDROPHOBIC.	
FT	DORAIN	474	482	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	483	503	M (N10) (POTENTIAL).	
FT	DORAIN	504	820	CYTOPLASMIC (POTENTIAL).	
FT	CARBOHYD	374	374	POTENTIAL.	
SQ	SEQUENCE	820	AA;	91467 MW;	CB3788F4 CRC32;
Query	Match	9	9.4%	Score 145; DB 1;	Length 820;
Best Local Similarity	27.3%			Pred. No. 9.97e-04;	
Matches	36;	Conservative	40;	Mismatches 45;	Indels 11;
				Gaps 9;	
Db	262	LVFGESLNDAVTYVLYHFEFASYDSYGVISD-IFLGFLSFFVVALGGFVYGVVV-GVI	319		
Db	82	LIFG--LL--AVIGHTFPIFAGFRKGKAVATSGAVIFGPIFCYLATIFGALYLGSM	137		
Oy	320	AAFTSRETSHIRVIEPLFF--LISYMAVYLSAELFHLSSIMALASGVYMRPYE-ANISH	377		
Oy	138	LSQ--VTTASIAATVYVLLFPLGFILSNYDSLF-IAIIAL-ASLIIIRHDNIARKN	194		
Db	378	KSHTTIKYFLKM	389		
Oy	195	KTENLVPWGLNL	206		

BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION.

- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

- PTM: PHOSPHORYLATED (POSSIBLE).

- SIMILARITY: BELONGS TO THE Na^+ / H^+ EXCHANGER FAMILY.

- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE Na^+ / H^+ EXCHANGERS VARY AMONG AUTHORS.

- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.

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CC	DR	EMBL: X68970; CAA48771.1;	DR	PFAM: PF00999; Na_H_Exchanger; 1;	KW	Transmembrane; Glycoprotein; Sodium transport; Transport; Symport; Multigene family; Phosphorylation.	FT DOMAIN	1	12	CYTOSMERIC (POTENTIAL).
							FT DOMAIN	1	13	A (M1) HYDROPHOBIC.
							FT DOMAIN	3	32	CYTOSMERIC (POTENTIAL).
							FT DOMAIN	33	105	B (M2) HYDROPHOBIC.
							FT DOMAIN	106	127	CYTOSMERIC (POTENTIAL).
							FT DOMAIN	128	130	C (M3) (POTENTIAL).
							FT TRANSMEM	131	150	EXTRACELLULAR (POTENTIAL).
							FT DOMAIN	151	162	EXTRACELLULAR (POTENTIAL).
							FT TRANSMEM	163	183	D (M4) (POTENTIAL).
							FT DOMAIN	184	188	CYTOSMERIC (POTENTIAL).
							FT TRANSMEM	189	210	E (M5) (POTENTIAL).
							FT DOMAIN	211	230	EXTRACELLULAR (POTENTIAL).
							FT TRANSMEM	231	251	F (M6A) (POTENTIAL).
							FT DOMAIN	252	260	CYTOSMERIC (POTENTIAL).
							FT TRANSMEM	261	282	G (M6B) (POTENTIAL).
							FT DOMAIN	283	301	EXTRACELLULAR (POTENTIAL).
							FT TRANSMEM	302	322	H (M6) (POTENTIAL).
							FT DOMAIN	323	336	CYTOSMERIC (POTENTIAL).
							FT TRANSMEM	337	357	I (M7) (POTENTIAL).
							FT DOMAIN	358	388	EXTRACELLULAR (POTENTIAL).
							FT TRANSMEM	389	410	J (M8) (POTENTIAL).
							FT DOMAIN	411	416	CYTOSMERIC (POTENTIAL).
							FT TRANSMEM	417	438	K (M9) (POTENTIAL).
							FT DOMAIN	439	452	EXTRACELLULAR (POTENTIAL).
							FT DOMAIN	453	473	L, HYDROPHOBIC.
							FT DOMAIN	474	482	EXTRACELLULAR (POTENTIAL).
							FT TRANSMEM	483	503	M (M10) (POTENTIAL).
							FT DOMAIN	504	822	CYTOSMERIC (POTENTIAL).
							FT BORDY	374	374	POTENTIAL.
SQ	SEQUENCE	822 AA;	92003 MW;	17073216 CRC32;						

P23791; 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
SIC91 OR NHE1.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metasoma; Chordata; Craniata; Vertebrata; Mammalia;
Butherzo; Lagomorpha; Leporidae; Oryctolagidae.
[1]
SEQUENCE FROM N.A.
STRAIN=NEW ZEALAND WHITE; TISSUE=ILEAL VILLUS;
MEDLINE: 91293066.
TSEDE C.-M., MA A.-I., YANG V.-W., WATSON A.-J.-M., LEVINE S.,
MONTROSE M.-H., PORTER J., SARDET C., PODYSSEGUR J., DONOWITZ
"Molecular cloning and expression of a cDNA encoding the rabbit
villus cell basolateral membrane Na⁺/H⁺ exchanger."
EMBO J. 10:1957-1967(1991).
[2]
SEQUENCE FROM N.A.

RA	ORLOWSKI J., KANDASAMY R.A., SHULL G.E.;	Qy	138 ISLSS-VTASIAAV-IGVLLPPF-GFGLSNSYDSLW-IAIILAL-ASLIIIRHKDNJARIKK 194
RT	Molecular cloning of putative members of the Na/H exchanger gene family. cDNA cloning, deduced amino acid sequence, and mRNA tissue expression of the rat Na/H exchanger NHE-1 and two structurally related proteins.;	Db	378 KSHTTIVYFLK 389
RT	J. Biol. Chem. 267:9331-9339(1992).	Qy	195 KTENLYPGNLN 206
RL	CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION.	Search completed: Wed Mar 8 10:23:31 2000	
CC	CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	Job time : 14 secs.	
CC	CC -1- TISSUE SPECIFICITY: NOT TISSUE SPECIFIC.		
CC	CC -1- PTM: PHOSPHORYLATED (POSSIBLE).		
CC	CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.		
CC	CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.		
CC	CC -1- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.		
CC	CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.ebi.ac.uk/announce/ or send an email to license@ebi.ac.uk).		
CC	CC -1- DR FBML: M85299; AAA98479.1; -		
DR	PIR: A40204; A40204.		
DR	PFAM: PF00599; Na_H_Exchanger; 1.		
KW	Multigene family; Glycoprotein; Sodium transport; Transport; Symport; KW Multigene family; Phosphorylation.		
KW	FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).		
FT	FT DOMAIN 13 32 A (M1) HYDROPHOBIC.		
FT	FT DOMAIN 33 105 CYTOPLASMIC (POTENTIAL).		
FT	FT DOMAIN 106 127 B (M2) HYDROPHOBIC.		
FT	FT DOMAIN 128 130 CYTOPLASMIC (POTENTIAL).		
FT	FT TRANSMEM 131 150 C (M3) (POTENTIAL).		
FT	FT DOMAIN 151 162 EXTRACELLULAR (POTENTIAL).		
FT	FT TRANSMEM 163 183 D (M4) (POTENTIAL).		
FT	FT DOMAIN 184 188 CYTOPLASMIC (POTENTIAL).		
FT	FT TRANSMEM 189 210 E (M5) (POTENTIAL).		
FT	FT DOMAIN 211 230 EXTRACELLULAR (POTENTIAL).		
FT	FT TRANSMEM 231 251 F (M5A) (POTENTIAL).		
FT	FT DOMAIN 252 260 CYTOPLASMIC (POTENTIAL).		
FT	FT TRANSMEM 261 282 G (M5B) (POTENTIAL).		
FT	FT DOMAIN 283 301 EXTRACELLULAR (POTENTIAL).		
FT	FT TRANSMEM 302 322 H (M6) (POTENTIAL).		
FT	FT DOMAIN 323 336 CYTOPLASMIC (POTENTIAL).		
FT	FT TRANSMEM 337 357 I (M7) (POTENTIAL).		
FT	FT DOMAIN 358 388 EXTRACELLULAR (POTENTIAL).		
FT	FT TRANSMEM 389 410 J (M8) (POTENTIAL).		
FT	FT DOMAIN 411 416 CYTOPLASMIC (POTENTIAL).		
FT	FT TRANSMEM 417 438 K (M9) (POTENTIAL).		
FT	FT DOMAIN 439 452 EXTRACELLULAR (POTENTIAL).		
FT	FT DOMAIN 453 473 L, HYDROPHOBIC.		
FT	FT DOMAIN 474 482 EXTRACELLULAR (POTENTIAL).		
FT	FT TRANSMEM 483 503 M (M10) (POTENTIAL).		
FT	FT DOMAIN 504 820 CYTOPLASMIC (POTENTIAL).		
FT	CARBOHYD 374 374 POTENTIAL.		
SQ	SEQUENCE 820 AA; 91.647 MW; 5286E311 CRC32;		
Query	Match 9.0%	Score 139;	DB 1; Length 820;
Best Local Matches	Similarity 27.38;	Pre. 0.420e-03;	No. 3;
Matches	36; Conservative 39; Mismatches 46;	Indels 11; Gaps 9;	
Db	262 LVFGESLINDAVTVVLLHFFEEASYEVNGISD-IFLGFLSFFVVSIGFVGVV-GVI 319		
Qy	82 LIFG--LJ--AVIHTPPIFAFKGGRAVATSGAVIFGAFIFCLYLAIFGALYGSW 137		
Db	320 AAFTSRETFSHIRVIEPLVF--LYSMAYLSAELFHLSGGIMALIASGVMPYVE-ANISH 377		